



## SEQUENCE LISTING

<110> Guarante, Leonard  
Imai, Shin-ichiro  
Armstrong, Christopher

<120> METHODS FOR IDENTIFYING AGENTS WHICH  
ALTER HISTONE PROTEIN ACETYLATION, DECREASE AGING, INCREASE  
LIFESPAN

<130> 0050.1618-000

<140> 09/461,580  
<141> 1999-12-15

<160> 35

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35 40 45  
Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Gly Cys Glu Ala Ala  
50 55 60  
Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala  
65 70 75 80  
Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly  
85 90 95  
Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe  
100 105 110  
Asp Asp Asp Glu Gly Glu Glu Asp Glu Ala Ala Ala Ala Ala  
115 120 125  
Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu  
130 135 140  
Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Asp Arg Thr  
145 150 155 160  
Ser His Ala Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro  
165 170 175  
Tyr Thr Phe Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr  
180 185 190  
Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp  
195 200 205  
Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro  
210 215 220

Lys Arg Lys Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys  
 225 230 235 240  
 Leu Leu Gln Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val  
 245 250 255  
 Ser Val Ser Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr  
 260 265 270  
 Ala Arg Leu Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met  
 275 280 285  
 Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe  
 290 295 300  
 Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys  
 305 310 315 320  
 Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr  
 325 330 335  
 Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu  
 340 345 350  
 Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr  
 355 360 365  
 Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val  
 370 375 380  
 Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys  
 385 390 395 400  
 Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg  
 405 410 415  
 Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly  
 420 425 430  
 Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro  
 435 440 445  
 His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu  
 450 455 460  
 His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu  
 465 470 475 480  
 Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro  
 485 490 495  
 Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu  
 500 505 510  
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 515 520 525  
 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile  
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 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu  
 545 550 555 560  
 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr  
 565 570 575  
 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala  
 580 585 590  
 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu  
 595 600 605  
 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser  
 610 615 620  
 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr  
 625 630 635 640  
 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu  
 645 650 655

Ser	Ser	Ser	Ser	Cys	Gly	Ser	Asn	Ser	Asp	Ser	Gly	Thr	Cys	Gln	Ser
				660		665							670		
Pro	Ser	Leu	Glu	Glu	Pro	Leu	Glu	Asp	Glu	Ser	Glu	Ile	Glu	Glu	Phe
					675		680						685		
Tyr	Asn	Gly	Leu	Glu	Asp	Asp	Thr	Glu	Arg	Pro	Glu	Cys	Ala	Gly	Gly
					690		695				700				
Ser	Gly	Phe	Gly	Ala	Asp	Gly	Gly	Asp	Gln	Glu	Val	Val	Asn	Glu	Ala
					705		710			715			720		
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Ser

<210> 2

<211> 272

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

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Ile	Asp	His	Phe	Ile	Gln	Lys	Leu	His	Thr	Ala	Arg	Lys	Ile	Leu	Val
					20			25					30		
Leu	Thr	Gly	Ala	Gly	Val	Ser	Thr	Ser	Leu	Gly	Ile	Pro	Asp	Phe	Arg
					35.			40				45			
Ser	Ser	Glu	Gly	Phe	Tyr	Ser	Lys	Ile	Lys	His	Leu	Gly	Leu	Asp	Asp
					50			55			60				
Pro	Gln	Asp	Val	Phe	Asn	Tyr	Asn	Ile	Phe	Met	His	Asp	Pro	Ser	Val
					65			70		75		80			
Phe	Tyr	Asn	Ile	Ala	Asn	Met	Val	Leu	Pro	Pro	Glu	Lys	Ile	Tyr	Ser
					85			90			95				
Pro	Leu	His	Ser	Phe	Ile	Lys	Met	Leu	Gln	Met	Lys	Gly	Lys	Leu	Leu
					100			105			110				
Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	Glu	Ser	Tyr	Ala	Gly	Ile
					115			120			125				
Ser	Thr	Asp	Lys	Leu	Val	Gln	Cys	His	Gly	Ser	Phe	Ala	Thr	Ala	Thr
					130			135			140				
Cys	Val	Thr	Cys	His	Trp	Asn	Leu	Pro	Gly	Glu	Arg	Ile	Phe	Asn	Lys
					145			150		155		160			
Ile	Arg	Asn	Leu	Glu	Leu	Pro	Leu	Cys	Pro	Tyr	Cys	Tyr	Lys	Lys	Arg
					165			170			175				
Arg	Glu	Tyr	Phe	Pro	Glu	Gly	Tyr	Asn	Asn	Lys	Val	Gly	Val	Ala	Ala
					180			185			190				
Ser	Gln	Gly	Ser	Met	Ser	Glu	Arg	Pro	Pro	Tyr	Ile	Leu	Asn	Ser	Tyr
					195			200			205				
Gly	Val	Leu	Lys	Pro	Asp	Ile	Thr	Phe	Phe	Gly	Glu	Ala	Leu	Pro	Asn
					210			215		220					
Lys	Phe	His	Lys	Ser	Ile	Arg	Glu	Asp	Ile	Leu	Glu	Cys	Asp	Leu	Leu
					225			230		235			240		
Ile	Cys	Ile	Gly	Thr	Ser	Leu	Lys	Val	Ala	Pro	Val	Ser	Glu	Ile	Val
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Asn	Met	Val	Pro	Ser	His	Val	Pro	Gln	Val	Leu	Ile	Asn	Arg	Asp	Pro
					260			265			270				

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<213> *Saccharomyces cerevisiae*

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Ile Asp His Phe Thr Ala Thr Leu Arg Asn Ala Lys Lys Ile Leu Val  
20              25              30  
Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg  
35              40              45  
Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly Leu Glu Asp  
50              55              60  
Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp Pro Ser Val  
65              70              75              80  
Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn Met Tyr Ser  
85              90              95  
Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly Lys Leu Leu  
100             105             110  
Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile  
115             120             125  
Asp Pro Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Ser  
130             135             140  
Cys Val Thr Cys His Trp Gln Ile Pro Gly Glu Lys Ile Phe Glu Asn  
145             150             155             160  
Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Gln Lys Arg  
165             170             175  
Lys Gln Tyr Phe Pro Met Ser Asn Gly Asn Asn Thr Val Gln Thr Asn  
180             185             190  
Ile Asn Phe Asn Ser Pro Ile Leu Lys Ser Tyr Gly Val Leu Lys Pro  
195             200             205  
Asp Met Thr Phe Phe Gly Glu Ala Leu Pro Ser Arg Phe His Lys Thr  
210             215             220  
Ile Arg Lys Asp Ile Leu Glu Cys Asp Leu Leu Ile Cys Ile Gly Thr  
225             230             235             240  
Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val Asn Met Val Pro Ser  
245             250             255  
His Val Pro Gln Ile Leu Ile Asn Arg Asp Met  
260             265

<210> 4  
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<212> PRT  
<213> *Mus musculus*

<400> 4  
Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp  
1               5               10               15  
Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys  
20              25              30  
Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro  
35              40              45

Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe  
   50                       55                       60  
 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg  
   65                       70                       75                       80  
 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly  
   85                       90                       95  
 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys  
   100                      105                       110  
 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu  
   115                      120                       125  
 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala  
   130                      135                       140  
 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val  
   145                      150                       155                       160  
 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro  
   165                      170                       175  
 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly  
   180                      185                       190  
 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp  
   195                      200                       205  
 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro  
   210                      215                       220  
 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu  
   225                      230                       235                       240  
 Ile Asn Arg Glu Pro  
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<210> 5  
 <211> 237  
 <212> PRT  
 <213> Escherichia coli

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 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu  
   20                      25                       30  
 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Phe Ala Arg Asn  
   35                      40                       45  
 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln  
   50                      55                       60  
 Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu  
   65                      70                       75                       80  
 Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp  
   85                      90                       95  
 Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly  
   100                     105                       110  
 Glu Leu Leu Lys Val Arg Cys Ser Gln Ser Gly Gln Ile Leu Glu Trp  
   115                     120                       125  
 Asn Gly Asp Val Met Pro Glu Asp Lys Cys His Cys Cys Gln Phe Pro  
   130                     135                       140  
 Ala Pro Leu Arg Pro His Val Val Trp Phe Gly Glu Met Pro Leu Gly  
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<213> Artificial Sequence
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<220>  
<223> Synthetic Peptide

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Arg His Arg Cys  
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<210> 8  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Peptide

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His Ser Cys

<210> 9  
<211> 128  
<212> PRT  
<213> Mus musculus

<400> 9  
Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp  
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35 40 45  
Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln  
50 55 60  
Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys Glu  
65 70 75 80  
Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu Gln  
85 90 95  
Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala Thr  
100 105 110  
Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val Arg  
115 120 125

<210> 10  
<211> 128  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 10  
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Phe Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly Leu  
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Asp Asp Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp Pro  
35 40 45  
Ser Val Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys Ile  
50 55 60  
Tyr Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly Lys  
65 70 75 80  
Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala  
85 90 95  
Gly Ile Ser Thr Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr  
100 105 110  
Ala Thr Cys Val Thr Cys His Trp Asn Leu Pro Gly Glu Arg Ile Phe  
115 120 125

<210> 11  
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<212> PRT  
<213> Saccharomyces cerevisiae

<400> 11

Ala Ile Asn Lys Val Leu Cys Thr Arg Leu Arg Leu Ser Asn Phe Phe  
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 Thr Ile Asp His Phe Ile Gln Lys Leu His Thr Ala Arg Lys Ile Leu  
 20 25 30  
 Val Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe  
 35 40 45  
 Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly Leu Asp  
 50 55 60  
 Asp Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp Pro Ser  
 65 70 75 80  
 Val Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys Ile Tyr  
 85 90 95  
 Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly Lys Leu  
 100 105 110  
 Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly  
 115 120 125  
 Ile Ser Thr Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala  
 130 135 140  
 Thr Cys Val Thr Cys His Trp Asn Leu Pro Gly Glu Arg Ile Phe Asn  
 145 150 155 160  
 Lys Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Lys Lys  
 165 170 175  
 Arg Arg Glu Tyr Phe Pro Glu Gly Tyr Asn Asn Lys Val Gly Val Ala  
 180 185 190  
 Ala Ser Gln Gly Ser Met Ser Glu Arg Pro Pro Tyr Ile Leu Asn Ser  
 195 200 205  
 Tyr Gly Val Leu Lys Pro Asp Ile Thr Phe Phe Gly Glu Ala Leu Pro  
 210 215 220  
 Asn Lys Phe His Lys Ser Ile Arg Glu Asp Ile Leu Glu Cys Asp Leu  
 225 230 235 240  
 Leu Ile Cys Ile Gly Thr Ser Leu Lys Val Ala Pro Val Ser Glu Ile  
 245 250 255  
 Val Asn Met Val Pro Ser His Val Pro Gln Val Leu Ile Asn Arg Asp  
 260 265 270  
 Pro Val Lys His Ala Glu Phe Asp Leu Ser Leu Leu Gly Tyr Cys Asp  
 275 280 285  
 Asp Ile Ala Ala Met Val Ala Gln Lys Cys Gly Trp Thr Ile Pro His  
 290 295 300  
 Lys Lys Trp Asn Asp Leu Lys Asn Lys Asn Phe Lys Cys Gln Glu Lys  
 305 310 315 320  
 Asp Lys Gly Val Tyr Val Val Thr Ser Asp Glu His Pro Lys Thr Leu  
 325 330 335

<210> 12  
 <211> 327  
 <212> PRT  
 <213> Mus musculus

<400> 12  
 Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp  
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 Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys  
 20 25 30

Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro  
       35                  40                  45  
 Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe  
       50                  55                  60  
 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg  
       65                  70                  75                  80  
 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly  
       85                  90                  95  
 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys  
       100                105                110  
 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu  
       115                120                125  
 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala  
       130                135                140  
 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val  
       145                150                155                160  
 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro  
       165                170                175  
 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly  
       180                185                190  
 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp  
       195                200                205  
 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro  
       210                215                220  
 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu  
       225                230                235                240  
 Ile Asn Arg Glu Pro Leu Pro His Leu His Phe Asp Val Glu Leu Leu  
       245                250                255  
 Gly Asp Cys Asp Val Ile Ile Asn Glu Leu Cys His Arg Leu Gly Gly  
       260                265                270  
 Glu Tyr Ala Lys Leu Cys Cys Asn Pro Val Lys Leu Ser Glu Ile Thr  
       275                280                285  
 Glu Lys Pro Pro Arg Pro Gln Lys Glu Leu Val His Leu Ser Glu Leu  
       290                295                300  
 Pro Pro Thr Pro Leu His Ile Ser Glu Asp Ser Ser Ser Pro Glu Arg  
       305                310                315                320  
 Thr Val Pro Gln Asp Ser Ser  
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<210> 13  
<211> 237  
<212> PRT  
<213> Escherichia coli

<400> 13  
 Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser  
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 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu  
       20                25                30  
 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Pro Ala Arg Asn  
       35                40                45  
 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln  
       50                55                60

Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu  
 65 70 75 80  
 Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp  
       85 90 95  
 Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly  
       100 105 110  
 Glu Leu Leu Lys Val Arg Cys Ser Gln Ser Gly Gln Ile Leu Glu Trp  
       115 120 125  
 Asn Gly Asp Val Met Pro Glu Asp Lys Cys His Cys Cys Gln Phe Pro  
       130 135 140  
 Ala Pro Leu Arg Pro His Val Val Trp Phe Gly Glu Met Pro Leu Gly  
 145 150 155 160  
 Met Asp Glu Ile Tyr Met Ala Leu Ser Met Ala Asp Ile Phe Ile Ala  
       165 170 175  
 Ile Gly Thr Ser Gly His Val Tyr Pro Ala Ala Gly Phe Val His Glu  
       180 185 190  
 Ala Lys Leu His Gly Ala His Thr Val Glu Leu Asn Leu Glu Pro Ser  
       195 200 205  
 Gln Val Gly Asn Glu Phe Glu Glu Lys His Tyr Gly Pro Ala Ser Gln  
       210 215 220  
 Val Val Pro Glu Phe Val Asp Lys Phe Leu Lys Gly Leu  
 225 230 235

<210> 14  
 <211> 106  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 14  
 Ile Leu Val Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro  
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 Asp Phe Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly  
       20 25 30  
 Leu Asp Asp Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp  
       35 40 45  
 Pro Ser Val Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys  
       50 55 60  
 Ile Tyr Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly  
 65 70 75 80  
 Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr  
       85 90 95  
 Ala Gly Ile Ser Thr Asp Lys Leu Val Gln  
       100 105

<210> 15  
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 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 15  
 Ile Leu Val Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro  
 1 5 10 15

Asp Phe Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly  
     20                25                30  
 Leu Glu Asp Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp  
     35                40                45  
 Pro Ser Val Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn  
     50                55                60  
 Met Tyr Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly  
     65                70                75                80  
 Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr  
     85                90                95  
 Ala Gly Ile Asp Pro Asp Lys Leu Val Gln  
     100               105

<210> 16  
 <211> 107  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 16  
 Val Ile Phe Met Val Gly Ala Gly Ile Ser Thr Ser Cys Gly Ile Pro  
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 Asp Phe Arg Ser Pro Gly Thr Gly Leu Tyr His Asn Leu Ala Arg Leu  
     20                25                30  
 Lys Leu Pro Tyr Pro Glu Ala Val Phe Asp Val Asp Phe Phe Gln Ser  
     35                40                45  
 Asp Pro Leu Pro Phe Tyr Thr Leu Ala Lys Glu Leu Tyr Pro Gly Asn  
     50                55                60  
 Phe Arg Pro Ser Lys Phe His Tyr Leu Leu Lys Leu Phe Gln Asp Lys  
     65                70                75                80  
 Asp Val Leu Lys Arg Val Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg  
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 Gln Ala Gly Val Lys Asp Asp Leu Ile Ile Glu  
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<210> 17  
 <211> 131  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 17  
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 Asp Phe Arg Ser Ser Asp Gly Leu Tyr Asp Leu Val Lys Lys Asp Cys  
     20                25                30  
 Ser Gln Tyr Trp Ser Ile Lys Ser Gly Arg Glu Met Phe Asp Ile Ser  
     35                40                45  
 Leu Phe Arg Asp Asp Phe Lys Ile Ser Ile Phe Ala Lys Phe Met Glu  
     50                55                60  
 Arg Leu Tyr Ser Asn Val Gln Leu Ala Lys Pro Thr Lys Thr His Lys  
     65                70                75                80  
 Phe Ile Ala His Leu Lys Asp Arg Asn Lys Leu Leu Arg Cys Tyr Thr  
     85                90                95

Gln Asn Ile Asp Gly Leu Glu Glu Ser Ile Gly Leu Thr Leu Ser Asn  
           100               105               110  
 Arg Lys Leu Pro Leu Thr Ser Phe Ser Ser His Trp Lys Asn Leu Asp  
           115               120               125  
 Val Val Gln  
           130

<210> 18  
<211> 117  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 18  
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 Asp Phe Arg Ser Ser Glu Gly Ile Phe Ser Thr Val Asn Gly Gly Ser  
     20               25               30  
 Gly Lys Asp Leu Phe Asp Tyr Asn Arg Val Tyr Gly Asp Glu Ser Met  
     35               40               45  
 Ser Leu Lys Phe Asn Gln Leu Met Val Ser Leu Phe Arg Leu Ser Lys  
     50               55               60  
 Asn Cys Gln Pro Thr Lys Phe His Glu Met Leu Asn Glu Phe Ala Arg  
     65               70               75               80  
 Asp Gly Arg Leu Leu Arg Leu Tyr Thr Gln Asn Ile Asp Gly Leu Asp  
     85               90               95  
 Thr Gln Leu Pro His Leu Ser Thr Asn Val Pro Leu Ala Lys Pro Ile  
     100               105               110  
 Pro Ser Thr Val Gln  
     115

<210> 19  
<211> 106  
<212> PRT  
<213> *Mus musculus*

<400> 19  
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     20               25               30  
 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg  
     35               40               45  
 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly  
     50               55               60  
 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys  
     65               70               75               80  
 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu  
     85               90               95  
 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln  
     100               105

<210> 20

<211> 107  
<212> PRT  
<213> Mus musculus

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His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys  
35 40 45  
His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln  
50 55 60  
Phe Lys Pro Thr Ile Cys His Tyr Phe Ile Arg Leu Leu Lys Glu Lys  
65 70 75 80  
Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg  
85 90 95  
Val Ala Gly Leu Glu Pro Gln Asp Leu Val Glu  
100 105

<210> 21  
<211> 86  
<212> PRT  
<213> Mus musculus

<400> 21  
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1 5 10 15  
Glu Ala Ile Phe Glu Leu Gly Phe Phe His Asn Pro Lys Pro Phe  
20 25 30  
Phe Met Leu Ala Lys Glu Leu Tyr Pro Gly His Tyr Arg Pro Asn Val  
35 40 45  
Thr His Tyr Phe Leu Arg Leu Leu His Asp Lys Glu Leu Leu Arg  
50 55 60  
Leu Tyr Thr Gln Asn Ile Asp Gly Leu Glu Arg Ala Ser Gly Ile Pro  
65 70 75 80  
Ala Ser Lys Leu Val Glu  
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<210> 22  
<211> 85  
<212> PRT  
<213> Unknown

<220>  
<223> Unknown Protein

<400> 22  
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Asp Phe Arg Gly Pro His Gly Val Trp Thr Met Glu Glu Arg Gly Leu  
20 25 30

Ala Pro Lys Phe Asp Thr Thr Phe Glu Asn Ala Arg Pro Ser Lys Thr  
     35                        40                        45  
 His Met Ala Leu Val Gln Leu Glu Arg Met Gly Phe Leu Ser Phe Leu  
     50                        55                        60  
 Val Ser Gln Asn Val Asp Gly Leu Asp Val Arg Ser Gly Phe Pro Arg  
     65                        70                        75                        80  
 Asp Lys Leu Ala Glu  
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<210> 23  
 <211> 71  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Unknown Protein

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     20                        25                        30  
 Pro Ile Gln His Ile Asp Phe Val Pro Val Leu Arg Ser Ala Ser Gly  
     35                        40                        45  
 Thr Trp Pro Glu Asn Leu Trp Ala Gly Leu Asn Ser Pro Leu Thr Asn  
     50                        55                        60  
 Pro Thr Gln His Thr Trp Leu  
     65                        70

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 <211> 75  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Unknown Protein

<400> 24  
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 Thr Phe Arg Gly Ala Gly Gly Tyr Trp Arg Lys Trp Gln Ala Gln Asp  
     20                        25                        30  
 Leu Ala Thr Pro Gln Ala Phe Ala Arg Asn Pro Ser Gln Val Trp Glu  
     35                        40                        45  
 Phe Tyr His Tyr Arg Arg Glu Val Met Arg Ser Lys Glu Pro Asn Pro  
     50                        55                        60  
 Gly His Leu Ala Ile Ala Gln Cys Glu Ala Arg  
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<210> 25  
 <211> 3869  
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (48) . . . (2261)

<400> 25

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Glu Val Ala Leu Ala Leu Gln Ala Ala Gly Ser Pro Ser Ala Ala Ala
      5           10          15

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gcc atg gag gcc gcg tcg cag ccg gcg gac gag ccg ctc cgc aag agg 152
Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu Arg Lys Arg
   20          25          30          35

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ccc cgc cga gac ggg cct ggc ctc ggg cgc agc ccg ggc gag ccg agc 200  
 Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly Glu Pro Ser  
 40 45 50

gca gca gtg gcg ccg gcg gcc gcg ggg tgt gag gcg gcg agc gcc gcg 248  
Ala Ala Val Ala Pro Ala Ala Gly Cys Glu Ala Ala Ser Ala Ala  
55 60 65

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gcc ccg gcg gcg ctg tgg cgg gag gcg gca ggg gcg gcg gcg gcg agc gcg 296
Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala Ala Ser Ala
    70           75           80

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gag cg<sup>g</sup> gag gcc cc<sup>g</sup> gc<sup>g</sup> ac<sup>g</sup> g<sup>cc</sup> gt<sup>g</sup> g<sup>cc</sup> g<sup>gg</sup> g<sup>a</sup>c g<sup>g</sup>ga g<sup>a</sup>c a<sup>a</sup>t g<sup>gg</sup>g 344  
 Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly Asp Asn Gly  
           85                  90                  95

tcc ggc ctg cgg cg<sub>g</sub> gag cc<sub>g</sub> agg gc<sub>g</sub> gct gac gac ttc gac gac gac 392  
 Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe Asp Asp Asp Asp  
 100 105 110 115

gag ggc gag gag gac gag gcg gcg gcg gca gcg gcg gcg gca gcg 440  
 Glu Gly Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala  
                   120                 125                 130

atc ggc tac cga gac aac ctc ctg ttg acc gat gga ctc ctc act aat 488  
 Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu Leu Thr Asn  
           135              140              145

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ggc ttt cat tcc tgt gaa agt gat gac gat gac aga acg tca cac gcc 536
Gly Phe His Ser Cys Glu Ser Asp Asp Asp Asp Arg Thr Ser His Ala
      150           155           160

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agc tct agt gac tgg act ccg cgg ccg cgg ata ggt cca tat act ttt 584  
Ser Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe  
165 170 175

gtt cag caa cat ctc atg att ggc acc gat cct cga aca att ctt aaa		632	
Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys			
180	185	195	
gat tta tta cca gaa aca att cct cca cct gag ctg gat gat atg acg		680	
Asp Leu Leu Pro Glu Thr Ile Pro Pro Glu Leu Asp Asp Met Thr			
200	205	210	
ctg tgg cag att gtt att aat atc ctt tca gaa cca cca aag cgg aaa		728	
Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys			
215	220	225	
aaa aga aaa gat atc aat aca att gaa gat gct gtg aag tta ctg cag		776	
Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln			
230	235	240	
gag tgt aaa aag ata ata gtt ctg act gga gct ggg gtt tct gtc tcc		824	
Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser			
245	250	255	
tgt ggg att cct gac ttc aga tca aga gac ggt atc tat gct cgc ctt		872	
Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu			
260	265	270	275
gcg gtg gac ttc cca gac ctc cca gac cct caa gcc atg ttt gat att		920	
Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile			
280	285	290	
gag tat ttt aga aaa gac cca aga cca ttc ttc aag ttt gca aag gaa		968	
Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu			
295	300	305	
ata tat ccc gga cag ttc cag ccg tct ctg tgt cac aaa ttc ata gct		1016	
Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala			
310	315	320	
ttg tca gat aag gaa gga aaa cta ctt cga aat tat actcaa aat ata		1064	
Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile			
325	330	335	
gat acc ttg gag cag gtt gca gga atc caa agg atc ctt cag tgt cat		1112	
Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His			
340	345	350	355
ggt tcc ttt gca aca gca tct tgc ctg att tgt aaa tac aaa gtt gat		1160	
Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp			
360	365	370	
tgt gaa gct gtt cgt gga gac att ttt aat cag gta gtt cct cgg tgc		1208	
Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys			
375	380	385	
cct agg tgc cca gct gat gag cca ctt gcc atc atg aag cca gag att		1256	
Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile			
390	395	400	

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tat gac aaa gat gaa gtt gac ctc ctc att gtt att gga tct tct ctg Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu 420 425 430 435	1352
aaa gtg aga cca gta gca cta att cca agt tct ata ccc cat gaa gtg Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val 440 445 450	1400
cct caa ata tta ata aat agg gaa cct ttg cct cat cta cat ttt gat Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu His Phe Asp 455 460 465	1448
gta gag ctc ctt gga gac tgc gat gtt ata att aat gag ttg tgt cat Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu Leu Cys His 470 475 480	1496
agg cta ggt ggt gaa tat gcc aaa ctt tgt tgt aac cct gta aag ctt Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro Val Lys Leu 485 490 495	1544
tca gaa att act gaa aaa cct cca cgc cca caa aag gaa ttg gtt cat Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu Leu Val His 500 505 510 515	1592
tta tca gag ttg cca cca aca cct ctt cat att tcg gaa gac tca agt Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu Asp Ser Ser 520 525 530	1640
tca cct gaa aga act gta cca caa gac tct tct gtg att gct aca ctt Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile Ala Thr Leu 535 540 545	1688
gta gac caa gca aca aac aac aat gtt aat gat tta gaa gta tct gaa Val Asp Gln Ala Thr Asn Asn Val Asn Asp Leu Glu Val Ser Glu 550 555 560	1736
tca agt tgt gtg gaa gaa aaa cca caa gaa gta cag act agt agg aat Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr Ser Arg Asn 565 570 575	1784
gtt gag aac att aat gtg gaa aat cca gat ttt aag gct gtt ggt tcc Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala Val Gly Ser 580 585 590 595	1832
agt act gca gac aaa aat gaa aga act tca gtt gca gaa aca gtg aga Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu Thr Val Arg 600 605 610	1880

aaa tgc tgg cct aat aga ctt gca aag gag cag att agt aag cg	gg	ctt	1928
Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser Lys Arg Leu			
615	620	625	
gag ggt aat caa tac ctg ttt gta cca cca aat cgt tac ata ttc cac			1976
Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr Ile Phe His			
630	635	640	
ggt gct gag gta tac tca gac tct gaa gat gac gtc ttg tcc tct agt			2024
Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser			
645	650	655	
tcc tgt ggc agt aac agt gac agt ggc aca tgc cag agt cca agt tta			2072
Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu			
660	665	670	675
gaa gaa ccc ttg gaa gat gaa agt gaa att gaa gaa ttc tac aat ggc			2120
Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly			
680	685	690	
ttg gaa gat gat acg gag agg ccc gaa tgt gct gga gga tct gga ttt			2168
Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Ser Gly Phe			
695	700	705	
gga gct gat gga ggg gat caa gag gtt gtt aat gaa gct ata gct aca			2216
Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala Ile Ala Thr			
710	715	720	
aga cag gaa ttg aca gat gta aac tat cca tca gac aaa tca taa			2261
Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys Ser *			
725	730	735	
cactattgaa gctgtccgga ttcatcgtt gctccaccag cattggaaac ttttagcatgt			2321
caaaaaaatg aatgtttact tttttttttt tttttttttt tttttttttt tttttttttt			2381
tagactggaa aatagattgt cttcttgat aattttctaaa gttccatcat ttctgtttgt			2441
acttgtacat tcaacactgt tggttgactt catcttcctt tcaaggttca tttgtatgt			2501
acattcgtat gtatgtataa tttttttttt tgcctaattttt gtttcaacct tttaaagttt			2561
tcaaaagcca ttggaaatgtt aatgttaaagg gaacagctta tctagaccaa agaatggtat			2621
ttcacacttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			2681
acttttattt ttaggacagt taactttta aacactggca ttttccaaaa cttgtggcag			2741
ctaaactttt aaaatcacag atgacttgc atgtgaggag tcagcacccgt gtctggagca			2801
ctaaaaactt gggctcagtg tttttttttt tttttttttt tttttttttt tttttttttt			2861
gacgtggtaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			2921
tttagttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			2981
ccattgtttt attaaatacc tatcactgtg tttttttttt tttttttttt tttttttttt			3041
actgccaaga tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3101
agagtgtaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3161
ttaaaatgtttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3221
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tccaaatgtttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3341
gggatcaatt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3401
gtcagtattttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt			3461
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cccagtttagg accattactg ccagaggaga aaagtattaa gtagctcatt tccctaccta			3581
aaagataact gaattttttt ggctacacta aagaatgcag tatattttttt tttccattttt			3641

catgatgtgt ttgtgctata gacaatattt taaattgaaa aatttgaaaa aaatttatttt 3701  
 tacagtgaag actgtttca gcttttttta tattgtacat agacttttat gtaatctggc 3761  
 atatgtttt tagaccgttt aatgactgga ttatcttcct ccaacttttg aaatacaaaa 3821  
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<210> 26  
<211> 737  
<212> PRT  
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<400> 26  
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 35 40 45  
 Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Gly Cys Glu Ala Ala  
 50 55 60  
 Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala  
 65 70 75 80  
 Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly  
 85 90 95  
 Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe  
 100 105 110  
 Asp Asp Asp Glu Gly Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala  
 115 120 125  
 Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu  
 130 135 140  
 Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Asp Arg Thr  
 145 150 155 160  
 Ser His Ala Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro  
 165 170 175  
 Tyr Thr Phe Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr  
 180 185 190  
 Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp  
 195 200 205  
 Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro  
 210 215 220  
 Lys Arg Lys Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys  
 225 230 235 240  
 Leu Leu Gln Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val  
 245 250 255  
 Ser Val Ser Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr  
 260 265 270  
 Ala Arg Leu Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met  
 275 280 285  
 Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe  
 290 295 300  
 Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys  
 305 310 315 320  
 Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr  
 325 330 335  
 Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu  
 340 345 350

Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr  
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 Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val  
     370                       375                       380  
 Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys  
     385                       390                       395                   400  
 Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg  
     405                       410                       415  
 Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly  
     420                       425                       430  
 Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro  
     435                       440                       445  
 His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu  
     450                       455                       460  
 His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu  
     465                       470                       475                   480  
 Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro  
     485                       490                       495  
 Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu  
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 Leu Val His Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu  
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 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile  
     530                       535                       540  
 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu  
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 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr  
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 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala  
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 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu  
     595                       600                       605  
 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser  
     610                       615                       620  
 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr  
     625                       630                       635                   640  
 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu  
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 Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser  
     660                       665                       670  
 Pro Ser Leu Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe  
     675                       680                       685  
 Tyr Asn Gly Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly  
     690                       695                       700  
 Ser Gly Phe Gly Ala Asp Gly Asp Gln Glu Val Val Asn Glu Ala  
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 Ile Ala Thr Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys  
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gtc ccg agg gcc ccc acc ccg ttc cca tgg ccg agc cg <sup>g</sup> acc gat tca	95
Val Pro Arg Ala Pro Thr Pro Phe Pro Trp Pro Ser Arg Thr Asp Ser	
20 25 30	
gac tcg gac act gag gga gga gcc act ggt gga gag gca gag atg gac	143
Asp Ser Asp Thr Glu Gly Ala Thr Gly Glu Ala Glu Met Asp	
35 40 45	
ttc ctg agg aat tta ttc acc cag acc ctg ggc ctg ggt tcc caa aag	191
Phe Leu Arg Asn Leu Phe Thr Gln Thr Leu Gly Leu Gly Ser Gln Lys	
50 55 60	
gag cgt ctt cta gac gag ctg acc ctc gaa gga gtg aca cgc tac atg	239
Glu Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Thr Arg Tyr Met	
65 70 75	
cag agc gag cgc tgc cgc aag gtc atc tgt ttg gtg gga gcc gga atc	287
Gln Ser Glu Arg Cys Arg Lys Val Ile Cys Leu Val Gly Ala Gly Ile	
80 85 90 95	
tcc acg tcc gc <sup>g</sup> ggt atc cct gac ttc cgc tcc ccg tcc act ggc ctc	335
Ser Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu	
100 105 110	
tat gca aac ctg gag aag tac cac ctt cct tac cca gag gcc atc ttt	383
Tyr Ala Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe	
115 120 125	
gag atc agc tac ttc aag aaa cat ccg gaa ccc ttc ttt gcc ctt gcc	431
Glu Ile Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala Leu Ala	
130 135 140	
aag gag ctc tat ccc ggg cag ttc aag cca acc atc tgc cac tac ttc	479
Lys Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe	
145 150 155	
atc cgc ctg ctg aag gag aag ggg ctg ctg ctg cgc tgc tac acg cag	527
Ile Arg Leu Leu Lys Glu Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln	
160 165 170 175	
aac ata gac acg ctg gaa cga gtg gc <sup>g</sup> ggg ctg gag ccc cag gac ctg	575
Asn Ile Asp Thr Leu Glu Arg Val Ala Gly Leu Glu Pro Gln Asp Leu	
180 185 190	
gtg gag gcc cac ggc acc ttc tac aca tca cac tgt gtc aac acc tcc	623
Val Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Asn Thr Ser	
195 200 205	
tgc aga aaa gaa tac acg atg ggc tgg atg aaa gag aag att tct cag	671
Cys Arg Lys Glu Tyr Thr Met Gly Trp Met Lys Glu Lys Ile Ser Gln	
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35 40 45  
Leu Arg Asn Leu Phe Thr Gln Thr Leu Gly Leu Gly Ser Gln Lys Glu  
50 55 60  
Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Thr Arg Tyr Met Gln  
65 70 75 80  
Ser Glu Arg Cys Arg Lys Val Ile Cys Leu Val Gly Ala Gly Ile Ser  
85 90 95  
Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr  
100 105 110  
Ala Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu  
115 120 125  
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130 135 140  
Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Ile  
145 150 155 160  
Arg Leu Leu Lys Glu Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn  
165 170 175  
Ile Asp Thr Leu Glu Arg Val Ala Gly Leu Glu Pro Gln Asp Leu Val  
180 185 190  
Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Asn Thr Ser Cys  
195 200 205  
Arg Lys Glu Tyr Thr Met Gly Trp Met Lys Glu Lys Ile Ser Gln Lys  
210 215 220  
Gln Leu Pro Gly Val Ser Ser Val  
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